In the Claims

Please cancel claim 1. Please add new claims 2, 3 and 4 listed below.

Listing of claims:

1. (canceled)

2. (new) A process for identifying one or more bi-allelic markers linked to a bi-allelic genetic characteristic gene in a species of creatures, comprising the acts of:

a) choosing two or more bi-allelic covering markers so that a CL-F region is systematically covered by the two or more covering markers, the CL-F region being a collection of points on a two-dimensional plane, the two-dimensional plane having the two orthogonal dimensions of chromosomal location and least common allele frequency;

b) choosing a statistical linkage test based on allelic association for each covering marker;

c) choosing a sample of individuals for each covering marker ;

d) obtaining genotype data/sample allele frequency data for each covering marker and the sample chosen for each covering marker, and obtaining phenotype status data for the genetic characteristic for each individual in the sample chosen for each covering marker;

e) calculating evidence for linkage between each covering marker and the gene using the statistical linkage test based on allelic association chosen for each covering marker and the genotype data/sample allele frequency data for each covering marker and using the phenotype status data for the genetic characteristic for each individual in the sample chosen for each covering marker obtained in d); and

f) identifying those covering markers as linked to the genetic characteristic gene which show evidence for linkage based on the calculations of e).

3. (new) A process for obtaining genotype data/sample allele frequency data for each bi-allelic marker of a group of two or more bi-allelic covering markers in the chromosomal DNA of one or more individuals of a sample, each individual in the sample being a member of the same species, comprising:

a)determining information on the presence or absence of each allele of each bi-allelic marker of a group of two or more bi-allelic covering markers in the chromosomal DNA of one or more individuals of a sample, a CL-F region being systematically covered by the two or more bi-allelic covering markers, the CL-F region being a collection of points on a two-dimensional plane, the two-dimensional plane having the two orthogonal dimensions of chromosomal location and least common allele frequency; and

b) transforming the information of step a) into genotype data/sample allele frequency data for each marker of the group.

4. (new) One or more copies of a set of oligonucleotides, the set of oligonucleotides being complementary to a group of two or more bi-allelic covering markers of the same species, wherein the group of covering markers systematically cover a CL-F region, the CL-F region being a collection of points on a two-dimensional plane, the two-dimensional plane having the two orthogonal dimensions of chromosomal location and least common allele frequency.